

Chiara Romualdi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9475889/publications.pdf>

Version: 2024-02-01

172
papers

8,029
citations

44066

48
h-index

60616

81
g-index

178
all docs

178
docs citations

178
times ranked

13527
citing authors

#	ARTICLE	IF	CITATIONS
1	IDE6: a web tool for detection of differentially expressed genes in multiple tag sampling experiments. <i>Physiological Genomics</i> , 2003, 12, 159-162.	2.3	336
2	Detection of Cortical Inflammatory Lesions by Double Inversion Recovery Magnetic Resonance Imaging in Patients With Multiple Sclerosis. <i>Archives of Neurology</i> , 2007, 64, 1416.	4.5	282
3	Life at Depth: <i>Photobacterium profundum</i> Genome Sequence and Expression Analysis. <i>Science</i> , 2005, 307, 1459-1461.	12.6	266
4	Cortical lesion load associates with progression of disability in multiple sclerosis. <i>Brain</i> , 2012, 135, 2952-2961.	7.6	246
5	microRNA-181a has a critical role in ovarian cancer progression through the regulation of the epithelial-mesenchymal transition. <i>Nature Communications</i> , 2014, 5, 2977.	12.8	226
6	Inflammatory intrathecal profiles and cortical damage in multiple sclerosis. <i>Annals of Neurology</i> , 2018, 83, 739-755.	5.3	219
7	Cortical atrophy is relevant in multiple sclerosis at clinical onset. <i>Journal of Neurology</i> , 2007, 254, 1212-1220.	3.6	208
8	Patterns of Human Diversity, within and among Continents, Inferred from Biallelic DNA Polymorphisms. <i>Genome Research</i> , 2002, 12, 602-612.	5.5	188
9	graphite - a Bioconductor package to convert pathway topology to gene network. <i>BMC Bioinformatics</i> , 2012, 13, 20.	2.6	177
10	Association between miR-200c and the survival of patients with stage I epithelial ovarian cancer: a retrospective study of two independent tumour tissue collections. <i>Lancet Oncology</i> , The, 2011, 12, 273-285.	10.7	173
11	Ripening and Genotype Control Stilbene Accumulation in Healthy Grapes. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 11773-11785.	5.2	170
12	MAGIA, a web-based tool for miRNA and Genes Integrated Analysis. <i>Nucleic Acids Research</i> , 2010, 38, W352-W359.	14.5	150
13	Resistance to platinum-based chemotherapy is associated with epithelial to mesenchymal transition in epithelial ovarian cancer. <i>European Journal of Cancer</i> , 2013, 49, 520-530.	2.8	141
14	miR148b is a major coordinator of breast cancer progression in a relapse-associated microRNA signature by targeting ITGA5, ROCK1, PIK3CA, NRAS, and CSF1. <i>FASEB Journal</i> , 2013, 27, 1223-1235.	0.5	134
15	Widespread cortical thinning characterizes patients with MS with mild cognitive impairment. <i>Neurology</i> , 2010, 74, 321-328.	1.1	132
16	Microsatellite unstable gastrointestinal neuroendocrine carcinomas: a new clinicopathologic entity. <i>Endocrine-Related Cancer</i> , 2015, 22, 35-45.	3.1	126
17	Cortical lesions in primary progressive multiple sclerosis. <i>Neurology</i> , 2009, 72, 1330-1336.	1.1	124
18	Development of mussel mRNA profiling: Can gene expression trends reveal coastal water pollution?. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2006, 602, 121-134.	1.0	113

#	ARTICLE	IF	CITATIONS
19	MAGIA2: from miRNA and genes expression data integrative analysis to microRNA-transcription factor mixed regulatory circuits (2012 update). <i>Nucleic Acids Research</i> , 2012, 40, W13-W21.	14.5	110
20	Parallel protein and transcript profiles of FSHD patient muscles correlate to the D4Z4 arrangement and reveal a common impairment of slow to fast fibre differentiation and a general deregulation of MyoD-dependent genes. <i>Proteomics</i> , 2006, 6, 5303-5321.	2.2	105
21	Along signal paths: an empirical gene set approach exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013, 41, e19-e19.	14.5	105
22	Liver transcriptome analysis in gilthead sea bream upon exposure to low temperature. <i>BMC Genomics</i> , 2014, 15, 765.	2.8	96
23	Cognitive impairment predicts disability progression and cortical thinning in MS: An 8-year study. <i>Multiple Sclerosis Journal</i> , 2017, 23, 848-854.	3.0	88
24	parmigene: a parallel R package for mutual information estimation and gene network reconstruction. <i>Bioinformatics</i> , 2011, 27, 1876-1877.	4.1	82
25	The cortical damage, early relapses, and onset of the progressive phase in multiple sclerosis. <i>Neurology</i> , 2018, 90, e2107-e2118.	1.1	82
26	Evidence for relative cortical sparing in benign multiple sclerosis: a longitudinal magnetic resonance imaging study. <i>Multiple Sclerosis Journal</i> , 2009, 15, 36-41.	3.0	78
27	Characterizing genomic alterations in cancer by complementary functional associations. <i>Nature Biotechnology</i> , 2016, 34, 539-546.	17.5	78
28	Cortical pathology in multiple sclerosis patients with epilepsy: a 3 year longitudinal study. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2012, 83, 49-54.	1.9	75
29	Circulating miRNA landscape identifies miR-1246 as promising diagnostic biomarker in high-grade serous ovarian carcinoma: A validation across two independent cohorts. <i>Cancer Letters</i> , 2017, 388, 320-327.	7.2	73
30	Gene expression profiling in dysferlinopathies using a dedicated muscle microarray. <i>Human Molecular Genetics</i> , 2002, 11, 3283-3298.	2.9	70
31	Denervation in murine fast-twitch muscle: short-term physiological changes and temporal expression profiling. <i>Physiological Genomics</i> , 2006, 25, 60-74.	2.3	70
32	Direct generation of human naive induced pluripotent stem cells from somatic cells in microfluidics. <i>Nature Cell Biology</i> , 2019, 21, 275-286.	10.3	70
33	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses: Table 1.. <i>Nucleic Acids Research</i> , 2016, 44, D620-D623.	14.5	69
34	The changing clinical course of multiple sclerosis: A matter of gray matter. <i>Annals of Neurology</i> , 2013, 74, 76-83.	5.3	68
35	Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. <i>Neurogastroenterology and Motility</i> , 2020, 32, e13914.	3.0	68
36	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. <i>Genome Biology</i> , 2020, 21, 191.	8.8	67

#	ARTICLE	IF	CITATIONS
37	Magnetic resonance evidence of cerebellar cortical pathology in multiple sclerosis. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2010, 81, 401-404.	1.9	66
38	Differential gene expression profiling in genetic and multifactorial cardiovascular diseases. <i>Journal of Molecular and Cellular Cardiology</i> , 2006, 41, 934-948.	1.9	64
39	Single cell analysis reveals the involvement of the long non-coding RNA Pvt1 in the modulation of muscle atrophy and mitochondrial network. <i>Nucleic Acids Research</i> , 2019, 47, 1653-1670.	14.5	63
40	Gene set analysis exploiting the topology of a pathway. <i>BMC Systems Biology</i> , 2010, 4, 121.	3.0	62
41	lncRNAs as Novel Indicators of Patients' Prognosis in Stage I Epithelial Ovarian Cancer: A Retrospective and Multicentric Study. <i>Clinical Cancer Research</i> , 2017, 23, 2356-2366.	7.0	57
42	Development and validation of a gene expression oligo microarray for the gilthead sea bream (<i>Sparus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.8	55
43	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. <i>BMC Genomics</i> , 2008, 9, 630.	2.8	55
44	Morphology and evolution of cortical lesions in multiple sclerosis. A longitudinal MRI study. <i>NeuroImage</i> , 2008, 42, 1324-1328.	4.2	55
45	Transcriptomic Analysis of Single Isolated Myofibers Identifies miR-27a-3p and miR-142-3p as Regulators of Metabolism in Skeletal Muscle. <i>Cell Reports</i> , 2019, 26, 3784-3797.e8.	6.4	55
46	Detecting differentially expressed genes in multiple tag sampling experiments: comparative evaluation of statistical tests. <i>Human Molecular Genetics</i> , 2001, 10, 2133-2141.	2.9	54
47	miRNA Landscape in Stage I Epithelial Ovarian Cancer Defines the Histotype Specificities. <i>Clinical Cancer Research</i> , 2013, 19, 4114-4123.	7.0	53
48	Prognostic Relevance of Aberrant DNA Methylation in G1 and G2 Pancreatic Neuroendocrine Tumors. <i>Neuroendocrinology</i> , 2014, 100, 26-34.	2.5	53
49	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. <i>Human Molecular Genetics</i> , 2003, 12, 823-836.	2.9	51
50	Identification of high-grade serous ovarian cancer miRNA species associated with survival and drug response in patients receiving neoadjuvant chemotherapy: a retrospective longitudinal analysis using matched tumor biopsies. <i>Annals of Oncology</i> , 2016, 27, 625-634.	1.2	50
51	Altered glucose metabolism and proteolysis in pancreatic cancer cell conditioned myoblasts: searching for a gene expression pattern with a microarray analysis of 5000 skeletal muscle genes. <i>Gut</i> , 2004, 53, 1159-1166.	12.1	49
52	A modified LOESS normalization applied to microRNA arrays: a comparative evaluation. <i>Bioinformatics</i> , 2009, 25, 2685-2691.	4.1	49
53	Graphite Web: web tool for gene set analysis exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013, 41, W89-W97.	14.5	49
54	Analysis of Differential miRNA Expression in Primary Tumor and Stroma of Colorectal Cancer Patients. <i>BioMed Research International</i> , 2014, 2014, 1-8.	1.9	49

#	ARTICLE	IF	CITATIONS
55	Regional Distribution and Evolution of Gray Matter Damage in Different Populations of Multiple Sclerosis Patients. <i>PLoS ONE</i> , 2015, 10, e0135428.	2.5	49
56	Gene expression profiling identifies potential relevant genes in alveolar rhabdomyosarcoma pathogenesis and discriminates PAX3-FKHR positive and negative tumors. <i>International Journal of Cancer</i> , 2006, 118, 2772-2781.	5.1	48
57	The Human Adult Skeletal Muscle Transcriptional Profile Reconstructed by a Novel Computational Approach. <i>Genome Research</i> , 2000, 10, 344-349.	5.5	47
58	The <sc>CSF</sc> Profile Linked to Cortical Damage Predicts Multiple Sclerosis Activity. <i>Annals of Neurology</i> , 2020, 88, 562-573.	5.3	46
59	Aberrant DNA methylation profiles of inherited and sporadic colorectal cancer. <i>Clinical Epigenetics</i> , 2015, 7, 131.	4.1	45
60	Expression analysis of androgen-responsive genes in the prostate of veal calves treated with anabolic hormones. <i>Domestic Animal Endocrinology</i> , 2006, 30, 38-55.	1.6	44
61	Targeting p53 and histone methyltransferases restores exhausted CD8+ T cells in HCV infection. <i>Nature Communications</i> , 2020, 11, 604.	12.8	44
62	RAP: a new computer program for de novo identification of repeated sequences in whole genomes. <i>Bioinformatics</i> , 2005, 21, 582-588.	4.1	41
63	MIDAW: a web tool for statistical analysis of microarray data. <i>Nucleic Acids Research</i> , 2005, 33, W644-W649.	14.5	41
64	Wiring miRNAs to pathways: a topological approach to integrate miRNA and mRNA expression profiles. <i>Nucleic Acids Research</i> , 2014, 42, e96-e96.	14.5	41
65	Beneficial Bacteria Isolated from Grapevine Inner Tissues Shape <i>Arabidopsis thaliana</i> Roots. <i>PLoS ONE</i> , 2015, 10, e0140252.	2.5	41
66	A founder MYBPC3 mutation results in HCM with a high risk of sudden death after the fourth decade of life. <i>Journal of Medical Genetics</i> , 2015, 52, 338-347.	3.2	41
67	Disentangling the microRNA regulatory milieu in multiple myeloma: integrative genomics analysis outlines mixed miRNA-TF circuits and pathway-derived networks modulated in t(4;14) patients. <i>Oncotarget</i> , 2016, 7, 2367-2378.	1.8	41
68	Longitudinal analysis of immune cell phenotypes in early stage multiple sclerosis: distinctive patterns characterize MRI-active patients. <i>Brain</i> , 2006, 129, 1993-2007.	7.6	39
69	A-MADMAN: Annotation-based microarray data meta-analysis tool. <i>BMC Bioinformatics</i> , 2009, 10, 201.	2.6	38
70	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. <i>BMC Genomics</i> , 2006, 7, 287.	2.8	37
71	Profiling cancer gene mutations in longitudinal epithelial ovarian cancer biopsies by targeted next-generation sequencing: a retrospective study. <i>Annals of Oncology</i> , 2015, 26, 1363-1371.	1.2	37
72	Genome-wide study of salivary miRNAs identifies miR-423-5p as promising diagnostic and prognostic biomarker in oral squamous cell carcinoma. <i>Theranostics</i> , 2021, 11, 2987-2999.	10.0	37

#	ARTICLE	IF	CITATIONS
73	Impact of Host Genes and Strand Selection on miRNA and miRNA* Expression. PLoS ONE, 2011, 6, e23854.	2.5	37
74	Territorial male gobies respond aggressively to sneakers but do not adjust their sperm expenditure. Behavioral Ecology, 2005, 16, 1001-1007.	2.2	36
75	Expression profiling of skeletal muscle in young bulls treated with steroidal growth promoters. Physiological Genomics, 2009, 38, 138-148.	2.3	36
76	Gene flow and genetic diversity: a comparison of freshwater bryozoan populations in Europe and North America. Heredity, 2000, 85, 498-508.	2.6	35
77	Simplifying amino acid alphabets by means of a branch and bound algorithm and substitution matrices. Bioinformatics, 2002, 18, 1102-1108.	4.1	35
78	Integration Analysis of MicroRNA and mRNA Expression Profiles in Human Peripheral Blood Lymphocytes Cultured in Modeled Microgravity. BioMed Research International, 2014, 2014, 1-16.	1.9	35
79	Genome-wide Copy-number Alterations in Circulating Tumor DNA as a Novel Biomarker for Patients with High-grade Serous Ovarian Cancer. Clinical Cancer Research, 2021, 27, 2549-2559.	7.0	34
80	Low degree of cortical pathology is associated with benign course of multiple sclerosis. Multiple Sclerosis Journal, 2013, 19, 904-911.	3.0	32
81	Circulating Cell-Free DNA in Dogs with Mammary Tumors: Short and Long Fragments and Integrity Index. PLoS ONE, 2017, 12, e0169454.	2.5	32
82	Transcriptome Profiles of Human Visceral Adipocytes in Obesity and Colorectal Cancer Unravel the Effects of Body Mass Index and Polyunsaturated Fatty Acids on Genes and Biological Processes Related to Tumorigenesis. Frontiers in Immunology, 2019, 10, 265.	4.8	31
83	<i>metaGraphite</i> —a new layer of pathway annotation to get metabolite networks. Bioinformatics, 2019, 35, 1258-1260.	4.1	31
84	Pyrosequencing and de novo assembly of A ntarctic krill (<i>E uphausia superba</i>) transcriptome to study the adaptability of krill to climate-induced environmental changes. Molecular Ecology Resources, 2015, 15, 1460-1471.	4.8	30
85	FXVD5 (Dysadherin) upregulation predicts shorter survival and reveals platinum resistance in high-grade serous ovarian cancer patients. British Journal of Cancer, 2019, 121, 584-592.	6.4	30
86	Probability of conception on different days of the menstrual cycle: an ongoing exercise. , 1997, 13, 105-115.		29
87	Polymorphisms in von Willebrand factor gene promoter influence the glucocorticoid-induced increase in von Willebrand factor: the lesson learned from Cushing syndrome. British Journal of Haematology, 2008, 140, 230-235.	2.5	29
88	The self-morningness/eveningness (Self-ME): An extremely concise and totally subjective assessment of diurnal preference. Chronobiology International, 2015, 32, 1192-1200.	2.0	28
89	Improved detection of differentially expressed genes in microarray experiments through multiple scanning and image integration. Nucleic Acids Research, 2003, 31, 149e-149.	14.5	27
90	Revertant Fibers in the mdx Murine Model of Duchenne Muscular Dystrophy: An Age- and Muscle-Related Reappraisal. PLoS ONE, 2013, 8, e72147.	2.5	27

#	ARTICLE	IF	CITATIONS
91	Smokers and passive smokers gene expression profiles: Correlation with the DNA oxidation damage. <i>Free Radical Biology and Medicine</i> , 2007, 43, 415-422.	2.9	26
92	A leukemia-enriched cDNA microarray platform identifies new transcripts with relevance to the biology of pediatric acute lymphoblastic leukemia. <i>Haematologica</i> , 2005, 90, 890-8.	3.5	26
93	LINE-1 hypomethylation is associated to specific clinico-pathological features in Stage I non-small cell lung cancer. <i>Lung Cancer</i> , 2017, 108, 83-89.	2.0	25
94	KrillDB: A de novo transcriptome database for the Antarctic krill (<i>Euphausia superba</i>). <i>PLoS ONE</i> , 2017, 12, e0171908.	2.5	25
95	Genotype-specific mutations in the polymerase gene of hepatitis B virus potentially associated with resistance to oral antiviral therapy. <i>Antiviral Research</i> , 2012, 96, 422-429.	4.1	24
96	Synthesis of Mitochondrial DNA Precursors during Myogenesis, an Analysis in Purified C2C12 Myotubes*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5624-5635.	3.4	23
97	Paradoxical GH Increase During OGTT Is Associated With First-Generation Somatostatin Analog Responsiveness in Acromegaly. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 856-862.	3.6	23
98	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	3.6	23
99	Gray Matter Pathology in MS: A 3-Year Longitudinal Study in a Pediatric Population. <i>American Journal of Neuroradiology</i> , 2012, 33, 1507-1511.	2.4	22
100	Tissue-Specific Expression and Regulatory Networks of Pig MicroRNAome. <i>PLoS ONE</i> , 2014, 9, e89755.	2.5	22
101	High IGFBP2 Expression Correlates with Tumor Severity in Pediatric Rhabdomyosarcoma. <i>American Journal of Pathology</i> , 2011, 179, 2611-2624.	3.8	21
102	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. <i>Bioinformatics</i> , 2011, 27, 2127-2133.	4.1	21
103	Individual Radiosensitivity in Oncological Patients: Linking Adverse Normal Tissue Reactions and Genetic Features. <i>Frontiers in Oncology</i> , 2019, 9, 987.	2.8	21
104	Selection of multipotent cells and enhanced muscle reconstruction by myogenic macrophage-secreted factors. <i>Experimental Cell Research</i> , 2009, 315, 915-927.	2.6	20
105	A prognostic regulatory pathway in stage I epithelial ovarian cancer: new hints for the poor prognosis assessment. <i>Annals of Oncology</i> , 2016, 27, 1511-1519.	1.2	20
106	Disease genes and intracellular protein networks. <i>Physiological Genomics</i> , 2003, 15, 223-227.	2.3	19
107	A Systems Biology Approach to Characterize the Regulatory Networks Leading to Trabectedin Resistance in an In Vitro Model of Myxoid Liposarcoma. <i>PLoS ONE</i> , 2012, 7, e35423.	2.5	19
108	Increased NK Cell Count in Multiple Sclerosis Patients Treated With Dimethyl Fumarate: A 2-Year Longitudinal Study. <i>Frontiers in Immunology</i> , 2019, 10, 1666.	4.8	18

#	ARTICLE	IF	CITATIONS
109	Regional and temporal heterogeneity of epithelial ovarian cancer tumor biopsies: implications for therapeutic strategies. <i>Oncotarget</i> , 2016, 12, 2404-2417.	1.8	17
110	Usefulness of the Total Thrombusâ€­Formation Analysis System (Tâ€­TAS) in the diagnosis and characterization of von Willebrand disease. <i>Haemophilia</i> , 2016, 22, 949-956.	2.1	16
111	A data-driven network model of primary myelofibrosis: transcriptional and post-transcriptional alterations in CD34+ cells. <i>Blood Cancer Journal</i> , 2016, 6, e439-e439.	6.2	16
112	Novel genes, possibly relevant for molecular diagnosis or therapy of human rhabdomyosarcoma, detected by genomic expression profiling. <i>Gene</i> , 2005, 348, 65-71.	2.2	15
113	A comparison on effects of normalisations in the detection of differentially expressed genes. <i>BMC Bioinformatics</i> , 2009, 10, 61.	2.6	15
114	timeClip: pathway analysis for time course data without replicates. <i>BMC Bioinformatics</i> , 2014, 15, S3.	2.6	15
115	Changes in Accident & Emergency Visits and Return Visits in Relation to the Enforcement of Daylight Saving Time and Photoperiod. <i>Journal of Biological Rhythms</i> , 2018, 33, 555-564.	2.6	15
116	Multisite analysis of highâ€­grade serous epithelial ovarian cancers identifies genomic regions of focal and recurrent copy number alteration in 3q26.2 and 8q24.3. <i>International Journal of Cancer</i> , 2019, 145, 2670-2681.	5.1	15
117	Expression profiles of PRKG1, SDF2L1 and PPP1R12A are predictive and prognostic factors for therapy response and survival in highâ€­grade serous ovarian cancer. <i>International Journal of Cancer</i> , 2020, 147, 565-574.	5.1	15
118	A novel prognostic score to assess the risk of progression in relapsingâ€­remitting multiple sclerosis patients. <i>European Journal of Neurology</i> , 2021, 28, 2503-2512.	3.3	14
119	MicroRNA expression profiling with a droplet digital PCR assay enables molecular diagnosis and prognosis of cancers of unknown primary. <i>Molecular Oncology</i> , 2021, 15, 2732-2751.	4.6	14
120	PsiNorm: a scalable normalization for single-cell RNA-seq data. <i>Bioinformatics</i> , 2021, 38, 164-172.	4.1	14
121	NELL1, whose high expression correlates with negative outcomes, has different methylation patterns in alveolar and embryonal rhabdomyosarcoma. <i>Oncotarget</i> , 2017, 8, 33086-33099.	1.8	14
122	Global analysis of gene expression in mineralizing fish vertebra-derived cell lines: new insights into anti-mineralogenic effect of vanadate. <i>BMC Genomics</i> , 2011, 12, 310.	2.8	13
123	Global DNA methylation profiling uncovers distinct methylation patterns of protocadherin alpha4 in metastatic and non-metastatic rhabdomyosarcoma. <i>BMC Cancer</i> , 2016, 16, 886.	2.6	13
124	An aberrant microRNA signature in childhood T-cell lymphoblastic lymphoma affecting CDKN1B expression, NOTCH1 and growth factor signaling pathways. <i>Leukemia</i> , 2014, 28, 1909-1912.	7.2	12
125	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. <i>BMC Genomics</i> , 2009, 10, 596.	2.8	11
126	Microsatellite (GT) _n is part of the von Willebrand factor (VWF) promoter region that influences the glucocorticoid-induced increase in VWF in Cushing's syndrome. <i>Thrombosis Research</i> , 2010, 125, e275-e280.	1.7	11

#	ARTICLE	IF	CITATIONS
127	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. BMC Bioinformatics, 2007, 8, S23.	2.6	10
128	The effect of fingolimod on focal and diffuse grey matter damage in active MS patients. Journal of Neurology, 2018, 265, 2154-2161.	3.6	10
129	MOSClip: multi-omic and survival pathway analysis for the identification of survival associated gene and modules. Nucleic Acids Research, 2019, 47, e80.	14.5	10
130	Analysis of potential factors affecting allografts contamination at retrieval. Cell and Tissue Banking, 2017, 18, 539-545.	1.1	9
131	Transcriptional Characterization of Stage I Epithelial Ovarian Cancer: A Multicentric Study. Cells, 2019, 8, 1554.	4.1	9
132	Comprehensive Profiling of Hypoxia-Related miRNAs Identifies miR-23a-3p Overexpression as a Marker of Platinum Resistance and Poor Prognosis in High-Grade Serous Ovarian Cancer. Cancers, 2021, 13, 3358.	3.7	9
133	Correlation between Gene Expression and Clinical Data through Linear and Nonlinear Principal Components Analyses: Muscular Dystrophies as Case Studies. OMICS A Journal of Integrative Biology, 2009, 13, 173-184.	2.0	8
134	A systems biology approach to investigate the mechanism of action of trabectedin in a model of myelomonocytic leukemia. Pharmacogenomics Journal, 2018, 18, 56-63.	2.0	8
135	Zebrafish Mutant Lines Reveal the Interplay between nr3c1 and nr3c2 in the GC-Dependent Regulation of Gene Transcription. International Journal of Molecular Sciences, 2022, 23, 2678.	4.1	8
136	Copy number alterations in stage I epithelial ovarian cancer highlight three genomic patterns associated with prognosis. European Journal of Cancer, 2022, 171, 85-95.	2.8	8
137	Impact of probe annotation on the integration of miRNA-mRNA expression profiles for miRNA target detection. Nucleic Acids Research, 2010, 38, e97-e97.	14.5	7
138	Systems Biology Approach to the Dissection of the Complexity of Regulatory Networks in the S. scrofa Cardiocirculatory System. International Journal of Molecular Sciences, 2013, 14, 23160-23187.	4.1	7
139	Consequences of heat shock protein 72 (Hsp72) expression and activity on stress-induced apoptosis in CD30+ NPM-ALK+ anaplastic large-cell lymphomas. Leukemia, 2012, 26, 1375-1382.	7.2	6
140	rs4143815-PDL1, a New Potential Immunogenetic Biomarker of Biochemical Recurrence in Locally Advanced Prostate Cancer after Radiotherapy. International Journal of Molecular Sciences, 2019, 20, 2082.	4.1	6
141	A thorough annotation of the krill transcriptome offers new insights for the study of physiological processes. Scientific Reports, 2022, 12, .	3.3	6
142	Expression profiling characterization of laminin $\hat{I}\pm$ -2 positive MDC. Biochemical and Biophysical Research Communications, 2006, 350, 345-351.	2.1	5
143	Anticoagulant therapy for venous thromboembolism during pregnancy: a systematic review and a meta-analysis of the literature: a reply to a rebuttal. Journal of Thrombosis and Haemostasis, 2013, 11, 788-789.	3.8	5
144	A TGF- $\hat{I}2$ associated genetic score to define prognosis and platinum sensitivity in advanced epithelial ovarian cancer. Gynecologic Oncology, 2020, 156, 233-242.	1.4	5

#	ARTICLE	IF	CITATIONS
145	Circulating miR-185-5p as a Potential Biomarker for Arrhythmogenic Right Ventricular Cardiomyopathy. <i>Cells</i> , 2021, 10, 2578.	4.1	5
146	The power of word-frequency-based alignment-free functions: a comprehensive large-scale experimental analysis. <i>Bioinformatics</i> , 2022, 38, 925-932.	4.1	5
147	TRAIT (TRAnscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003, 19, 661-662.	4.1	4
148	Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. <i>BMC Bioinformatics</i> , 2011, 12, 92.	2.6	4
149	Graphical modeling for gene set analysis: A critical appraisal. <i>Biometrical Journal</i> , 2015, 57, 852-866.	1.0	4
150	SourceSet: A graphical model approach to identify primary genes in perturbed biological pathways. <i>PLoS Computational Biology</i> , 2019, 15, e1007357.	3.2	4
151	MyoData: An expression knowledgebase at single cell/nucleus level for the discovery of coding-noncoding RNA functional interactions in skeletal muscle. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4142-4155.	4.1	4
152	Similarity Measures Based on the Overlap of Ranked Genes Are Effective for Comparison and Classification of Microarray Data. <i>Journal of Computational Biology</i> , 2016, 23, 603-614.	1.6	3
153	simPATHy: a new method for simulating data from perturbed biological PATHways. <i>Bioinformatics</i> , 2017, 33, 456-457.	4.1	3
154	Sex identification from distinctive gene expression patterns in Antarctic krill (<i>Euphausia superba</i>). <i>Polar Biology</i> , 2019, 42, 2205-2217.	1.2	3
155	<i>NewWave</i> : a scalable R/Bioconductor package for the dimensionality reduction and batch effect removal of single-cell RNA-seq data. <i>Bioinformatics</i> , 2022, 38, 2648-2650.	4.1	3
156	Editorial: Multi-omic Data Integration in Oncology. <i>Frontiers in Oncology</i> , 2020, 10, 1768.	2.8	2
157	Pharmacogenetic score predicts overall survival, progression-free survival and platinum sensitivity in ovarian cancer. <i>Pharmacogenomics</i> , 2020, 21, 995-1010.	1.3	2
158	Statistical Tools for Gene Expression Analysis and Systems Biology and Related Web Resources. , 2009, , 181-205.		2
159	BrewerX enables allelic expression analysis of imprinted and X-linked genes from bulk and single-cell transcriptomes. <i>Communications Biology</i> , 2022, 5, 146.	4.4	2
160	Headrace tunnel of the El Alto hydropower project in Panama / Druckstollen des Wasserkraftprojekts El Alto in Panama. <i>Geomechanik Und Tunnelbau</i> , 2013, 6, 301-311.	0.3	1
161	Antimicrobial use and microbiological testing in district general hospital ICUs of the Veneto region of north-east Italy. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 1627-1638.	2.9	1
162	Su2003 “ Microencapsulated Sodium Butyrate Significantly Modifies the Microbiota in Patients with Inflammatory Bowel Disease Mimicking Prebiotic Activity and Proving Effects on the Treatment of the Disease. <i>Gastroenterology</i> , 2019, 156, S-687.	1.3	1

#	ARTICLE	IF	CITATIONS
163	881 MicroRNA Expression Profiling of Stage I Ovarian Carcinoma Reveals Signatures Characterizing the Different Tumor Grades and Histotypes. <i>European Journal of Cancer</i> , 2012, 48, S213.	2.8	0
164	PO-0974: Biomarkers of radiosensitivity for patient stratification and personalized radiotherapy treatment. <i>Radiotherapy and Oncology</i> , 2017, 123, S538-S539.	0.6	0
165	Cortical Thickness variability in Multiple Sclerosis: The role of lesion segmentation and filling. , 2017, , .		0
166	Advanced ovarian cancer: Is residual disease after debulking surgery affected by genetics factors involved in angiogenesis and immunity pathways?. <i>Annals of Oncology</i> , 2019, 30, v414-v415.	1.2	0
167	P.07.33 MICROENCAPSULATED SODIUM BUTYRATE SIGNIFICANTLY MODIFIES THE MICROBIOTA IN PATIENTS WITH INFLAMMATORY BOWEL DISEASE MIMICKING PREBIOTIC ACTIVITY AND PROVING EFFECTS ON THE TREATMENT OF THE DISEASE. <i>Digestive and Liver Disease</i> , 2019, 51, e236-e238.	0.9	0
168	Simulating gene silencing through intervention analysis. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2020, 69, 887-907.	1.0	0
169	Abstract B18: miRNA landscape analysis of stage I EOC, identifies miR-199a-5p associated to poor prognosis in grade 3 subgroup. , 2013, , .		0
170	Abstract B47: microRNA-181a plays a critical role in ovarian cancer progression through the regulation of epithelial-mesenchymal transition. , 2013, , .		0
171	Searching for the Source of Difference: A Graphical Model Approach. <i>Lecture Notes in Computer Science</i> , 2020, , 131-138.	1.3	0
172	miRNA bioinformatics and pathway analysis. , 2022, , 141-150.		0